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SEQUENCE LISTING

(1) GENERAL INFORMATION

- 70500
- (i) APPLICANT: Ullrich,, Axel
Gishizsky,, Mikhail
Sures,, Irman G.
- (ii) TITLE OF THE INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
TYROSINE KINASES
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York,
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: PatentIn, Ver 1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/426,509
(B) FILING DATE: 21-APR-1995
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/232,545
(B) FILING DATE: 22-APR-1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Coruzzi, Laura A
(B) REGISTRATION NUMBER: 30,742
(C) REFERENCE/DOCKET NUMBER: 7683-0074-999
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212-790-9090
(B) TELEFAX: 212-869-9741
(C) TELEX: 66141 PENNIE
- C'

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2000 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGCTCCAA	GTTGTGCAGC	CGGGACCGCC	TCGGGGTGTG	CAGCCGGCTC	GCGGAGGCCC	60
TCCTGGGGGC	GGGCGCGGGG	CGGCTCGGGG	GCGCCCCCTG	AGCAGAAAAC	AGGAAGAACC	120
AGGCTCGGTC	CAGTGGCACC	CAGCTCCCTA	CCTCCTGTGC	CAGCCGCCTG	GCCTGTGGCA	180
GGCCATTCCC	AGCGTCCCCG	ACTGTGACCA	CTTGCTCAGT	GTGCCTCTCA	CCTGCCTCAG	240
TTTCCTCTG	GGGGGCGATG	GCGGGGCGAG	GCTCTCTGGT	TTCTGGCGG	GCATTTCACG	300

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C

GCTGTGATTC	TGCTGAGGAA	CTTCCCCGGG	TGAGCCCCCG	CTTCCTCCGA	GCCTGGCACC	360
CCCCTCCCGT	CTCAGCCAGG	ATGCCAACGA	GGCGCTGGGC	CCCGGGCACC	CAGTGTATCA	420
CCAAATGCGA	GCACACCCGC	CCCAAGCCAG	GGGAGCTGGC	CTTCCGCAAG	GGCGACGTGG	480
TCACCATCCT	GGAGGCCTGC	GAGAACAAGA	GCTGGTACCG	CGTCAAGCAC	CACACCAGTG	540
GACAGGAGGG	GCTGCTGGCA	GCTGGGGCGC	TGCGGGAGCG	GGAGGCCCTC	TCCGCAGACC	600
CCAAGCTCAG	CCTCATGCCG	TGGTTCCACG	GGAAGATCTC	GGGCCAGGAG	GCTGTCCAGC	660
AGCTGCAGCC	TCCCGAGGAT	GGGCTGTTCC	TGGTGCGGGA	GTCCGCGCGC	CACCCCGGCG	720
ACTACGTCCT	GTGCGTGAGC	TTTGGCCGCG	ACGTCATCCA	CTACCGCGTG	CTGCACCGCG	780
ACGGCCACCT	CACAATCGAT	GAGGCCGTGT	TCTTCTGCAA	CCTCATGGAC	ATGGTGGAGC	840
ATTACAGCAA	GGACAAGGGC	GCTATCTGCA	CCAAGCTGGT	GAGACCAAAG	CGGAAACACG	900
GGACCAAGTC	GGCCGAGGAG	GAGCTGGCCA	GGGCGGGCTG	GTTACTGAAC	CTGCAGCATT	960
TGACATTGGG	AGCACAGATC	GGAGAGGGAG	AGTTTGGAGC	TGTCCTGCAG	GGTGAGTACC	1020
TGGGGCAAAA	GGTGGCCGTG	AAGAATATCA	AGTGTGATGT	GACAGCCAG	GCCTTCCTGG	1080
ACGAGACGGC	CGTCATGACG	AAGATGCAAC	ACGAGAACCT	GGTGCCTCTC	CTGGGCGTGA	1140
TCCTGCACCA	GGGGCTGTAC	ATTGTTCATG	AGCACGTGAG	CAAGGGCAAC	CTGGTGAAC	1200
TTCTGCGGAC	CCGGGGTCTGA	GCCCTCGTGA	ACACCGCTCA	GCTCCTGCAG	TTTTCTCTGC	1260
ACGTGGCCGA	GGGCATGGAG	TACCTGGAGA	GCAAGAAGCT	TGTGCACCGC	GACCTGGCCG	1320
CCCGCAACAT	CCTGGTCTCA	GAGGACCTGG	TGGCCAAGGT	CAGCGACTTT	GGCCTGGCCA	1380
AAGCCGAGCG	GAAGGGGCTA	GACTCAAGCC	GGCTGCCCGT	CAAGTGGACG	GCGCCCGAGG	1440
CTCTCAAACA	CGGGAAGTTC	ACCAGCAAGT	CGGATGTCTG	GAGTTTTGGG	GTGCTGCTCT	1500
GGGAGGTCTT	CTCATATGGA	CGGGCTCCGT	ACCCTAAAAT	GTCACTGAAA	GAGGTGTCTG	1560
AGGCCGTGGA	GAAGGGGTAC	CGCATGGAAC	CCCCCGAGGG	CTGTCCAGGC	CCCGTGCACG	1620
TCCTCATGAG	CAGCTGCTGG	GAGGCAGAGC	CCGCCCCGCC	GCCACCCTTC	CGCAAAC	1680
CCGAGAAGCT	GGCCCGGGAG	CTACGCAGTG	CAGGTGCCCC	AGCCTCCGTC	TCAGGGCAGG	1740
ACGCCGACGG	CTCCACCTCG	CCCCGAAGCC	AGGAGCCCTG	ACCCACCCG	GTGGGGCCCT	1800
TGGCCCCAGA	GGACCGAGAG	AGTGGAGAGT	GCGGCGTGGG	GGCACTGACC	AGGCCCAAGG	1860
AGGGTCCAGG	CGGGCAAGTC	ATCCTCCTGG	TGCCACACAG	AGGGGCTGGC	CCACGTAGGG	1920
GGCTCTGGGC	GGCCCGTGGA	CACCCAGAC	CTGCGAAGGA	TGATCGCCCC	ATAAAGACGG	1980
ATTCTAAGGA	CTCTAAAAAA					2000

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Gly	Arg	Gly	Ser	Leu	Val	Ser	Trp	Arg	Ala	Phe	His	Gly	Cys
1				5					10					15	
Asp	Ser	Ala	Glu	Glu	Leu	Pro	Arg	Val	Ser	Pro	Arg	Phe	Leu	Arg	Ala
			20					25					30		
Trp	His	Pro	Pro	Pro	Val	Ser	Ala	Arg	Met	Pro	Thr	Arg	Arg	Trp	Ala
			35				40					45			
Pro	Gly	Thr	Gln	Cys	Ile	Thr	Lys	Cys	Glu	His	Thr	Arg	Pro	Lys	Pro
			50				55				60				
Gly	Glu	Leu	Ala	Phe	Arg	Lys	Gly	Asp	Val	Val	Thr	Ile	Leu	Glu	Ala
65					70				75					80	
Cys	Glu	Asn	Lys	Ser	Trp	Tyr	Arg	Val	Lys	His	His	Thr	Ser	Gly	Gln
				85					90					95	
Glu	Gly	Leu	Leu	Ala	Ala	Gly	Ala	Leu	Arg	Glu	Arg	Glu	Ala	Leu	Ser
			100					105					110		
Ala	Asp	Pro	Lys	Leu	Ser	Leu	Met	Pro	Trp	Phe	His	Gly	Lys	Ile	Ser
			115				120					125			
Gly	Gln	Glu	Ala	Val	Gln	Gln	Leu	Gln	Pro	Pro	Glu	Asp	Gly	Leu	Phe
			130			135					140				
Leu	Val	Arg	Glu	Ser	Ala	Arg	His	Pro	Gly	Asp	Tyr	Val	Leu	Cys	Val
145					150				155					160	
Ser	Phe	Gly	Arg	Asp	Val	Ile	His	Tyr	Arg	Val	Leu	His	Arg	Asp	Gly
				165				170						175	
His	Leu	Thr	Ile	Asp	Glu	Ala	Val	Phe	Phe	Cys	Asn	Leu	Met	Asp	Met
			180					185					190		
Val	Glu	His	Tyr	Ser	Lys	Asp	Lys	Gly	Ala	Ile	Cys	Thr	Lys	Leu	Val

195 200 205
 Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala Glu Glu Glu Leu Ala
 210 215 220
 Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu Thr Leu Gly Ala Gln
 225 230 235 240
 Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln Gly Glu Tyr Leu Gly
 245 250 255
 Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp Val Thr Ala Gln Ala
 260 265 270
 Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met Gln His Glu Asn Leu
 275 280 285
 Val Arg Leu Leu Gly Val Ile Leu His Gln Gly Leu Tyr Ile Val Met
 290 295 300
 Glu His Val Ser Lys Gly Asn Leu Val Asn Phe Leu Arg Thr Arg Gly
 305 310 315 320
 Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln Phe Ser Leu His Val
 325 330 335
 Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys Leu Val His Arg Asp
 340 345 350
 Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp Leu Val Ala Lys Val
 355 360 365
 Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys Gly Leu Asp Ser Ser
 370 375 380
 Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Lys His Gly Lys
 385 390 395 400
 Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
 405 410 415
 Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys Met Ser Leu Lys Glu
 420 425 430
 Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met Glu Pro Pro Glu Gly
 435 440 445
 Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu
 450 455 460
 Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg
 465 470 475 480
 Glu Leu Arg Ser Ala Gly Ala Pro Ala Ser Val Ser Gly Gln Asp Ala
 485 490 495
 Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro
 500 505

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCTTTTGT	CTTAGAGCTT	GAGAGTCAAA	GTTAAGGACC	CACATGTATA	CTTCGGCTCT	60
AGCGAGTCTA	AGGATGATAA	TATGGATACA	AAATCTATTC	TAGAAGAACT	TCTTCTCAAA	120
AGATCACAGC	AAAAGAAGAA	AATGTCACCA	AATAATTACA	AAGAACGGCT	TTTTGTTTTG	180
ACCAAAACAA	ACCTTTCCTA	CTATGAATAT	GACAAAATGA	AAAGGGGCAG	CAGAAAAGGA	240
TCCATTGAAA	TTAAGAAAAT	CAGATGTGTG	GAGAAAGTAA	ATCTCGAGGA	GCAGACGCCT	300
GTAGAGAGAC	AGTACCCATT	TCAGATTGTC	TATAAAGATG	GGCTTCTCTA	TGTCTATGCA	360
TCAAATGAAG	AGAGCCGAAG	TCAGTGGTTG	AAAGCATTAC	AAAAAGAGAT	AAGGGGTAAC	420
CCCCACCTGC	TGGTCAAGTA	CCATAGTGGG	TTCTTCGTGG	ACGGGAAGTT	CCTGTGTTGC	480
CAGCAGAGCT	GTAAAGCAGC	CCCAGGATGT	ACCCTCTGGG	AAGCATATGC	TAATCTGCAT	540
ACTGCAGTCA	ATGAAGAGAA	ACACAGAGTT	CCCACCTTCC	CAGACAGAGT	GCTGAAGATA	600
CCTCGGGCAG	TTCCTGTTCT	CAAAATGGAT	GCACCATCTT	CAAGTACCAC	TCTAGCCCAA	660
TATGACAACG	AATCAAAGAA	AACTATGGC	TCCCAGCCAC	CATCTTCAAG	TACCAGTCTA	720
GCGCAATATG	ACAGCAACTC	AAAGAAAATC	TATGGCTCCC	AGCCAAACTT	CAACATGCAG	780
TATATTCCAA	GGGAAGACTT	CCCTGACTGG	TGGCAAGTAA	GAAAACTGAA	AAGTAGCAGC	840
AGCAGTGAAG	ATGTTGCAAG	CAGTAACCAA	AAAGAAAGAA	ATGTGAATCA	CACCACCTCA	900
AAGATTTTCAT	GGGAATTCCC	TGAGTCAAGT	TCATCTGAAG	AAGAGGAAAA	CCTGGATGAT	960

TATGACTGGT	TTGCTGGTAA	CATCTCCAGA	TCACAATCTG	AACAGTTACT	CAGACAAAAG	1020
GGAAAAGAAG	GAGCATTTAT	GGTTAGAAAT	TCGAGCCAAG	TGGGAATGTA	CACAGTGTCC	1080
TTATTTAGTA	AGGCTGTGAA	TGATAAAAAA	GGAAGTGTCA	AACATTACCA	CGTGCATACA	1140
AATGCTGAGA	ACAAATTATA	CCTGGCAGAA	AACTACTGTT	TTGATTCCAT	TCCAAAGCTT	1200
ATTCATTATC	ATCAACACAA	TTCAGCAGGC	ATGATCACAC	GGCTCCGCCA	CCCTGTGTCA	1260
ACAAAGGCCA	ACAAGGTCCC	CGACTCTGTG	TCCCTGGGAA	ATGGAATCTG	GGAAGTGAAG	1320
AGAGAAGAGA	TTACCTTGTT	GAAGGAGCTG	GGAAGTGGCC	AGTTTGGAGT	GGTCCAGCTG	1380
GGCAAGTGGA	AGGGGCAGTA	TGATGTTGCT	GTTAAGATGA	TCAAGGAGGG	CTCCATGTCA	1440
GAAGATGAAT	TCTTTCAGGA	GGCCCAGACT	ATGATGAAAC	TCAGCCATCC	CAAGCTGGTT	1500
AAATTCTATG	GAGTGTGTTT	AAAGGAATAC	CCCATATACA	TAGTGACTGA	ATATATAAGC	1560
AATGGCTGCT	TGCTGAATTA	CCTGAGGAGT	CACGGAAAAG	GACTTGAACC	TTCCCAGCTC	1620
TTAGAAATGT	GCTACGATGT	CTGTGAAGGC	ATGGCCTTCT	TGGAGAGTCA	CCAATTTCATA	1680
CACCGGGACT	TGGCTGCTCG	TAAGTGCTTG	GTGGACAGAG	ATCTCTGTGT	GAAAGTATCT	1740
GACTTTGGAA	TGACAAGGTA	TGTTCTTGAT	GACCAGTATG	TCAGTTCAGT	CGGAACAAAG	1800
TTTCCAGTCA	AGTGGTCAGC	TCCAGAGGTG	TTTCATTACT	TCAAATACAG	CAGCAAGTCA	1860
GACGTATGGG	CATTTGGGAT	CCTGATGTGG	GAGGTGTTCA	GCCTGGGGAA	GCAGCCCTAT	1920
GACTTGTATG	ACAACCTCCA	GGTGGTTCTG	AAGGTCTCCC	AGGGCCACAG	GCTTTACCGG	1980
CCCCACCTGG	CATCGGACAC	CATCTACCAG	ATCATGTACA	GCTGCTGGCA	CGAGCTTCCA	2040
GAAAAGCGTC	CCACATTTC	GCAACTCCTG	TCTTCCATTG	AACCACTTCG	GGAAAAAGAC	2100
AAGCATTGAA	GAAGAAATTA	GGAGTGCTGA	TAAGAATGAA	TATAGATGCT	GGCCAGCATT	2160
TTCATTTCATT	TTAAGGAAAG	TAGCAAGGCA	TAATGTAATT	TAGCTAGTTT	TTAATAGTGT	2220
TCTCTGTATT	GTCTATTATT	TAGAAATGAA	CAAGGCAGGA	AACAAAAGAT	TCCCTTGAAA	2280
TTTAGGTCAA	ATTAGTAATT	TTGTTTATGC	TGCCCTTGAT	ATAACACTTT	CCAGCCTATA	2340
GCAGAAGCAC	ATTTTCAGAC	TGCAATATAG	AGACTGTGTT	CATGTGTAAA	GACTGAGCAG	2400
AACTGAAAAA	TTACTTATTG	GATATTCATT	CTTTTCTTTA	TATTGTTCATT	GTCACAACAA	2460
TTAAATATAC	TACCAAGTAC	AAAAAAAAAA	AAAAAAAAAA			2500

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Thr	Lys	Ser	Ile	Leu	Glu	Glu	Leu	Leu	Lys	Arg	Ser	Gln
1				5					10				15	
Gln	Lys	Lys	Lys	Met	Ser	Pro	Asn	Asn	Tyr	Lys	Glu	Arg	Leu	Phe
			20				25						30	Val
Leu	Thr	Lys	Thr	Asn	Leu	Ser	Tyr	Tyr	Glu	Tyr	Asp	Lys	Met	Lys
		35		40							45			Arg
Gly	Ser	Arg	Lys	Gly	Ser	Ile	Glu	Ile	Lys	Lys	Ile	Arg	Cys	Val
	50				55						60			Glu
Lys	Val	Asn	Leu	Glu	Glu	Gln	Thr	Pro	Val	Glu	Arg	Gln	Tyr	Pro
65				70					75					80
Gln	Ile	Val	Tyr	Lys	Asp	Gly	Leu	Leu	Tyr	Val	Tyr	Ala	Ser	Asn
			85				90						95	Glu
Glu	Ser	Arg	Ser	Gln	Trp	Leu	Lys	Ala	Leu	Gln	Lys	Glu	Ile	Arg
			100				105						110	Gly
Asn	Pro	His	Leu	Leu	Val	Lys	Tyr	His	Ser	Gly	Phe	Phe	Val	Asp
		115				120					125			Gly
Lys	Phe	Leu	Cys	Cys	Gln	Gln	Ser	Cys	Lys	Ala	Ala	Pro	Gly	Cys
	130				135						140			Thr
Leu	Trp	Glu	Ala	Tyr	Ala	Asn	Leu	His	Thr	Ala	Val	Asn	Glu	Glu
145				150					155					Lys
His	Arg	Val	Pro	Thr	Phe	Pro	Asp	Arg	Val	Leu	Lys	Ile	Pro	Arg
			165				170						175	Ala
Val	Pro	Val	Leu	Lys	Met	Asp	Ala	Pro	Ser	Ser	Ser	Thr	Thr	Leu
			180				185						190	Ala
Gln	Tyr	Asp	Asn	Glu	Ser	Lys	Lys	Asn	Tyr	Gly	Ser	Gln	Pro	Pro
		195				200						205		Ser
Ser	Ser	Thr	Ser	Leu	Ala	Gln	Tyr	Asp	Ser	Asn	Ser	Lys	Lys	Ile
	210					215								Tyr

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C

Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr Ile Pro Arg Glu Asp Phe
 225 230 235 240
 Pro Asp Trp Trp Gln Val Arg Lys Leu Lys Ser Ser Ser Ser Ser Glu
 245 250 255
 Asp Val Ala Ser Ser Asn Gln Lys Glu Arg Asn Val Asn His Thr Thr
 260 265 270
 Ser Lys Ile Ser Trp Glu Phe Pro Glu Ser Ser Ser Ser Glu Glu Glu
 275 280 285
 Glu Asn Leu Asp Asp Tyr Asp Trp Phe Ala Gly Asn Ile Ser Arg Ser
 290 295 300
 Gln Ser Glu Gln Leu Leu Arg Gln Lys Gly Lys Glu Gly Ala Phe Met
 305 310 315 320
 Val Arg Asn Ser Ser Gln Val Gly Met Tyr Thr Val Ser Leu Phe Ser
 325 330 335
 Lys Ala Val Asn Asp Lys Lys Gly Thr Val Lys His Tyr His Val His
 340 345 350
 Thr Asn Ala Glu Asn Lys Leu Tyr Leu Ala Glu Asn Tyr Cys Phe Asp
 355 360 365
 Ser Ile Pro Lys Leu Ile His Tyr His Gln His Asn Ser Ala Gly Met
 370 375 380
 Ile Thr Arg Leu Arg His Pro Val Ser Thr Lys Ala Asn Lys Val Pro
 385 390 395 400
 Asp Ser Val Ser Leu Gly Asn Gly Ile Trp Glu Leu Lys Arg Glu Glu
 405 410 415
 Ile Thr Leu Leu Lys Glu Leu Gly Ser Gly Gln Phe Gly Val Val Gln
 420 425 430
 Leu Gly Lys Trp Lys Gly Gln Tyr Asp Val Ala Val Lys Met Ile Lys
 435 440 445
 Glu Gly Ser Met Ser Glu Asp Glu Phe Phe Gln Glu Ala Gln Thr Met
 450 455 460
 Met Lys Leu Ser His Pro Lys Leu Val Lys Phe Tyr Gly Val Cys Ser
 465 470 475 480
 Lys Glu Tyr Pro Ile Tyr Ile Val Thr Glu Tyr Ile Ser Asn Gly Cys
 485 490 495
 Leu Leu Asn Tyr Leu Arg Ser His Gly Lys Gly Leu Glu Pro Ser Gln
 500 505 510
 Leu Leu Glu Met Cys Tyr Asp Val Cys Glu Gly Met Ala Phe Leu Glu
 515 520 525
 Ser His Gln Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val
 530 535 540
 Asp Arg Asp Leu Cys Val Lys Val Ser Asp Phe Gly Met Thr Arg Tyr
 545 550 555 560
 Val Leu Asp Asp Gln Tyr Val Ser Ser Val Gly Thr Lys Phe Pro Val
 565 570 575
 Lys Trp Ser Ala Pro Glu Val Phe His Tyr Phe Lys Tyr Ser Ser Lys
 580 585 590
 Ser Asp Val Trp Ala Phe Gly Ile Leu Met Trp Glu Val Phe Ser Leu
 595 600 605
 Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn Ser Gln Val Val Leu Lys
 610 615 620
 Val Ser Gln Gly His Arg Leu Tyr Arg Pro His Leu Ala Ser Asp Thr
 625 630 635 640
 Ile Tyr Gln Ile Met Tyr Ser Cys Trp His Glu Leu Pro Glu Lys Arg
 645 650 655
 Pro Thr Phe Gln Gln Leu Leu Ser Ser Ile Glu Pro Leu Arg Glu Lys
 660 665 670
 Asp Lys His
 675

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2770 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

C'
cont.

60

C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGACTGGT	CGAAAGACAG	GAACAGACTT	GAAACAGGGG	GAGAGCTCCT	GGCGAAACGA	60
AGACGTGGAG	GTTTTACCAG	GGATAAGAAG	AAAAGACACC	TTCCTAGTGA	GCAGCTGCCC	120
AGCTCCTGCT	CAGTTTTGCC	TCGGGGTAGC	ACCTCCAGCC	ACAGAAAGCA	AGCCGGTAAG	180
TCTCTCCAGG	TAGGACTTGC	TGCAACCCAG	CTGCTGGACT	GATCTGAAAC	GGGACTTTGC	240
ATACTCTCCG	AAGTATGGTG	AGTTGGTGCT	GACTTCAAAG	TTGCCTGGTG	AAGGAAGATA	300
AGGTGGATCG	CAGAGACTAA	GGGGAGAGGG	AGAAGCCCTG	CTCCTCTTCT	CCCCACCAAG	360
GCACAATGAG	CAACATCTGT	CAGAGGCTCT	GGGAGTACCT	AGAACCCTAT	CTCCCCTGTT	420
TGTCCACGGA	GGCAGACAAG	TCAACCGTGA	TTGAAAATCC	AGGGGCCCTT	TGCTCTCCCC	480
AGTCACAGAG	GCATGGCCAC	TACTTTGTGG	CTTTGTTTGA	TTACCAGGCT	CGGACTGCTG	540
AGGACTTGAG	CTTCCGAGCA	GGTGACAAAC	TTCAAGTTCT	GGACACTTTG	CATGAGGGCT	600
GGTGGTTTGC	CAGACACTTG	GAGAAAAGAC	GAGATGGCTC	CAGTCAGCAA	CTACAAGGCT	660
ATATTCCTTC	TAACTACGTG	GCTGAGGACA	GAAGCCTACA	GGCAGAGCCG	TGGTTCTTTG	720
GAGCAATCGG	AAGATCAGAT	GCAGAGAAAC	AACTATTATA	TTCAGAAAAC	AAGACCGGTT	780
CCTTTCTAAT	CAGAGAAAAGT	GAAAGCCAAA	AAGGAGAATT	CTCTCTTTCA	GTTTTAGATG	840
GAGCAGTTGT	AAAACACTAC	AGAATTAAAA	GACTGGATGA	AGGGGGATTT	TTTCTCACGC	900
GAAGAAGAAT	CTTTTCAACA	CTGAACGAAT	TTGTGAGCCA	CTACACCAAG	ACAAGTGACG	960
GCCTGTGTGT	CAAGCTGGGG	AAACCATGCT	TAAAGATCCA	GGTCCCAGCT	CCATTTGATT	1020
TGTCGTATAA	AACCGTGGAC	CAATGGGAGA	TAGACCGCAA	CTCCATACAG	CTTCTGAAGC	1080
GATTGGGATC	TGGTCAGTTT	GGCGAAGTAT	GGGAAGGTCT	GTGGAACAAT	ACCACTCCAG	1140
TAGCAGTGAA	AACATTAAAA	CCAGGTTCAA	TGGATCCAAA	TGACTTCCTG	AGGGAGGCAC	1200
AGATAATGAA	GAACCTAAGA	CATCCAAAGC	TTATCCAGCT	TTATGCTGTT	TGCACTTTAG	1260
AAGATCCAAT	TTATATTATT	ACAGAGTTGA	TGAGACATGG	AAGTCTGCAA	GAATATCTCC	1320
AAAATGACAC	TGGATCAAAA	ATCCATCTGA	CTCAACAGGT	AGACATGGCG	GCACAGGTTG	1380
CCTCTGGAAT	GGCCTATCTG	GAGTCTCGGA	ACTACATTCA	CAGAGATCTG	GCTGCCAGAA	1440
ATGTCCTCGT	TGGTGAACAT	AATATCTACA	AAGTAGCAGA	TTTTGGACTT	GCCAGAGTTT	1500
TTAAGGTAGA	TAATGAAGAC	ATCTATGAAT	CTAGACACGA	AATAAAGCTG	CCGGTGAAGT	1560
GGACTGCGCC	CGAAGCCATT	CGTAGTAATA	AATTCAGCAT	TAAGTCCGAT	GTATGGTCAT	1620
TTGGAATCCT	TCTTTATGAA	ATCATTACTT	ATGGCAAAAT	GCCTTACAGT	GGTATGACAG	1680
GTGCCCAGGT	AATCCAGATG	TTGGCTCAAA	ACTATAGACT	TCCGCAACCA	TCCAAC TGTC	1740
CACAGCAATT	TTACAACATC	ATGTTGGAGT	GCTGGAATGC	AGAGCCTAAG	GAACGACCTA	1800
CATTTGAGAC	ACTGCGTTGG	AAACTTGAAG	ACTATTTTGA	AACAGACTCT	TCATATTTCAG	1860
ATGCAAATAA	CTTCATAAGA	TGAACACTGG	AGAAGAATAT	CAAATAATAA	AGTAGCAAAA	1920
CAAATTCAAA	TAATCCATTC	CAAAATACAA	TGTTATCAAC	CAACTGCACA	ATCAGTTTAT	1980
CCTGACATAT	TCAAGTGATA	GGATAAAGTT	GGCCATGTAT	TATGAAAAAG	ATTATTTGTG	2040
CATTTTATTG	ACTGGGCAAC	ACTGCAGGAC	AGTCAAGGTC	ATATATAATT	GCTCACTGCC	2100
TGGAAAATTA	AGCACACTAA	ACCAAGTTAT	TTTTCTTTTT	AAGAGATACT	TACATTTCCA	2160
TTTATTGTTT	GAAATGTCGC	GATCAAGAGA	ATCAACAGAT	GATAGTCCAA	TTTTTTACTCA	2220
GTGATGACTG	TGTAGCATTT	TCCTGTTTAC	TGATTAGAGT	GGTTATTCAT	TATTCCTCAG	2280
ATTGCTGAAT	CCCATCAGGC	TGTTATTATG	AAGGAATTTG	ATTGCTTTGC	TGCACAGCAG	2340
GACCTGTGCT	TTGAGATTTT	TTTTTCTCTT	TTAAAATATC	CTGTAACTAC	AATGATGGTA	2400
AAGCCATGTT	AAATGACTTG	ATTGTACTTG	GAGTAATTGC	ACATTTTTTT	CTATGCATAA	2460
AAAAATGATG	CAGCTGTTGA	GAAAACGAAG	TCTTTTTTCAT	TTTGCAGAAG	GAAATGATGG	2520
AATTTTTCTG	TACTTCAGTA	TGTGTCAACT	GAGAGTCATA	TACATTAGTT	TTAATCTCTT	2580
AATATTGAGA	ATCAGGTTGC	AAAACGGATG	AGTTATTATC	TATGGAAATG	TGAGAAATGT	2640
CTAATAGCCC	ATAAAGTCTG	AGAAATAGGT	ATCAAAATAG	TTTAGGAAAA	TGAGAGGAGA	2700
ACAGTAGGAT	TGCTGTGGCC	TAGACTTCTG	AGTAATTAAT	AAAGAAAAAG	AAGTACCAAA	2760
AAAAAAAAAA						2770

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Asn	Ile	Cys	Gln	Arg	Leu	Trp	Glu	Tyr	Leu	Glu	Pro	Tyr	Leu
1				5					10					15	
Pro	Cys	Leu	Ser	Thr	Glu	Ala	Asp	Lys	Ser	Thr	Val	Ile	Glu	Asn	Pro
			20					25					30		
Gly	Ala	Leu	Cys	Ser	Pro	Gln	Ser	Gln	Arg	His	Gly	His	Tyr	Phe	Val

Ala	Leu	Phe	Asp	Tyr	Gln	Ala	Arg	Thr	Ala	Glu	Asp	Leu	Ser	Phe	Arg
50						55					60				
Ala	Gly	Asp	Lys	Lys	Leu	Gln	Val	Leu	Asp	Thr	Leu	His	Glu	Gly	Trp
65					70					75					80
Trp	Phe	Ala	Arg	His	Leu	Glu	Lys	Arg	Arg	Asp	Gly	Ser	Ser	Gln	Gln
				85					90					95	
Leu	Gln	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Glu	Asp	Arg	Ser	Leu
			100					105					110		
Gln	Ala	Glu	Pro	Trp	Phe	Phe	Gly	Ala	Ile	Gly	Arg	Ser	Asp	Ala	Glu
		115					120					125			
Lys	Gln	Leu	Leu	Tyr	Ser	Glu	Asn	Lys	Thr	Gly	Ser	Phe	Leu	Ile	Arg
130						135					140				
Glu	Ser	Glu	Ser	Gln	Lys	Gly	Glu	Phe	Ser	Leu	Ser	Val	Leu	Asp	Gly
145					150					155					160
Ala	Val	Val	Lys	His	Tyr	Arg	Ile	Lys	Arg	Leu	Asp	Glu	Gly	Gly	Phe
				165					170					175	
Phe	Leu	Thr	Arg	Arg	Arg	Ile	Phe	Ser	Thr	Leu	Asn	Glu	Phe	Val	Ser
			180					185					190		
His	Tyr	Thr	Lys	Thr	Ser	Asp	Gly	Leu	Cys	Val	Lys	Leu	Gly	Lys	Pro
		195					200					205			
Cys	Leu	Lys	Ile	Gln	Val	Pro	Ala	Pro	Phe	Asp	Leu	Ser	Tyr	Lys	Thr
210						215					220				
Val	Asp	Gln	Trp	Glu	Ile	Asp	Arg	Asn	Ser	Ile	Gln	Leu	Leu	Lys	Arg
225					230					235					240
Leu	Gly	Ser	Gly	Gln	Phe	Gly	Glu	Val	Trp	Glu	Gly	Leu	Trp	Asn	Asn
				245					250					255	
Thr	Thr	Pro	Val	Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Ser	Met	Asp	Pro
			260					265					270		
Asn	Asp	Phe	Leu	Arg	Glu	Ala	Gln	Ile	Met	Lys	Asn	Leu	Arg	His	Pro
		275					280					285			
Lys	Leu	Ile	Gln	Leu	Tyr	Ala	Val	Cys	Thr	Leu	Glu	Asp	Pro	Ile	Tyr
290						295					300				
Ile	Ile	Thr	Glu	Leu	Met	Arg	His	Gly	Ser	Leu	Gln	Glu	Tyr	Leu	Gln
305					310					315					320
Asn	Asp	Thr	Gly	Ser	Lys	Ile	His	Leu	Thr	Gln	Gln	Tyr	Asp	Met	Ala
				325					330					335	
Ala	Gln	Val	Ala	Ser	Gly	Met	Ala	Tyr	Leu	Glu	Ser	Arg	Asn	Tyr	Ile
			340					345					350		
His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Gly	Glu	His	Asn	Ile
		355					360					365			
Tyr	Lys	Val	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Val	Phe	Lys	Val	Asp	Asn
370						375					380				
Glu	Asp	Ile	Tyr	Glu	Ser	Arg	His	Glu	Ile	Lys	Leu	Pro	Val	Lys	Trp
385					390					395					400
Thr	Ala	Pro	Glu	Ala	Ile	Arg	Ser	Asn	Lys	Phe	Ser	Ile	Lys	Ser	Asp
				405					410					415	
Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu	Tyr	Glu	Ile	Ile	Thr	Tyr	Gly	Lys
			420					425					430		
Met	Pro	Tyr	Ser	Gly	Met	Thr	Gly	Ala	Gln	Val	Ile	Gln	Met	Leu	Ala
		435					440					445			
Gln	Asn	Tyr	Arg	Leu	Pro	Gln	Pro	Ser	Asn	Cys	Pro	Gln	Gln	Phe	Tyr
450						455					460				
Asn	Ile	Met	Leu	Glu	Cys	Trp	Asn	Ala	Glu	Pro	Lys	Glu	Arg	Pro	Thr
465					470					475					480
Phe	Glu	Thr	Leu	Arg	Trp	Lys	Leu	Glu	Asp	Tyr	Phe	Glu	Thr	Asp	Ser
				485					490					495	
Ser	Tyr	Ser	Asp	Ala	Asn	Asn	Phe	Ile	Arg						
			500					505							

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
1 5 10 15
Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
20 25 30
Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
35 40 45
Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
50 55 60
Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
65 70 75 80
Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
85 90 95
Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
100 105 110
Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
115 120 125
Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
130 135 140
Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
145 150 155 160
Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
165 170 175
Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
180 185 190
Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
195 200 205
Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
210 215 220
Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
225 230 235 240
Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
245 250 255
Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
260 265 270
Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
275 280 285
Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
290 295 300
Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
305 310 315 320
Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
325 330 335
Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
340 345 350
Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
355 360 365
Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
370 375 380
Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
385 390 395 400
Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
405 410 415
Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
420 425 430
Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
435 440 445
His Leu
450

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 659 amino acids

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(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ala	Ala	Val	Ile	Leu	Glu	Ser	Ile	Phe	Leu	Lys	Arg	Ser	Gln	Gln
1				5					10					15	
Lys	Lys	Lys	Thr	Ser	Pro	Leu	Asn	Phe	Lys	Lys	Arg	Leu	Phe	Leu	Leu
			20					25					30		
Thr	Val	His	Lys	Leu	Ser	Tyr	Tyr	Glu	Tyr	Asp	Phe	Glu	Arg	Gly	Arg
		35					40					45			
Arg	Gly	Ser	Lys	Lys	Gly	Ser	Ile	Asp	Val	Glu	Lys	Ile	Thr	Cys	Val
	50					55					60				
Glu	Thr	Val	Val	Pro	Glu	Lys	Asn	Pro	Pro	Pro	Glu	Arg	Gln	Ile	Pro
65					70					75					80
Arg	Arg	Gly	Glu	Glu	Ser	Ser	Glu	Met	Glu	Gln	Ile	Ser	Ile	Ile	Glu
				85					90					95	
Arg	Phe	Pro	Tyr	Pro	Phe	Gln	Val	Val	Tyr	Asp	Glu	Gly	Pro	Leu	Tyr
			100					105					110		
Val	Phe	Ser	Pro	Thr	Glu	Glu	Leu	Arg	Lys	Arg	Trp	Ile	His	Gln	Leu
		115					120					125			
Lys	Asn	Val	Ile	Arg	Tyr	Asn	Ser	Asp	Leu	Val	Gln	Lys	Tyr	His	Pro
	130					135					140				
Cys	Phe	Trp	Ile	Asp	Gly	Gln	Tyr	Leu	Cys	Cys	Ser	Gln	Thr	Ala	Lys
145					150					155					160
Asn	Ala	Met	Gly	Cys	Gln	Ile	Leu	Glu	Asn	Arg	Asn	Gly	Ser	Leu	Lys
			165						170					175	
Pro	Gly	Ser	Ser	His	Arg	Lys	Thr	Lys	Lys	Pro	Leu	Pro	Pro	Thr	Pro
			180					185					190		
Glu	Glu	Asp	Gln	Ile	Leu	Lys	Lys	Pro	Leu	Pro	Pro	Glu	Pro	Ala	Ala
		195					200					205			
Ala	Pro	Val	Ser	Thr	Ser	Glu	Leu	Lys	Lys	Val	Val	Ala	Leu	Tyr	Asp
	210					215					220				
Tyr	Met	Pro	Met	Asn	Ala	Asn	Asp	Leu	Gln	Leu	Arg	Lys	Gly	Asp	Glu
225				230						235					240
Tyr	Phe	Ile	Leu	Glu	Glu	Ser	Asn	Leu	Pro	Trp	Trp	Arg	Ala	Arg	Asp
			245						250					255	
Lys	Asn	Gly	Gln	Glu	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Thr	Glu	Ala
			260					265					270		
Glu	Asp	Ser	Ile	Glu	Met	Tyr	Glu	Trp	Tyr	Ser	Lys	His	Met	Thr	Arg
		275					280					285			
Ser	Gln	Ala	Glu	Gln	Leu	Leu	Lys	Gln	Glu	Gly	Lys	Glu	Gly	Gly	Phe
	290					295					300				
Ile	Val	Arg	Asp	Ser	Ser	Lys	Ala	Gly	Lys	Tyr	Thr	Val	Ser	Val	Phe
305				310						315					320
Ala	Lys	Ser	Thr	Gly	Asp	Pro	Gln	Gly	Val	Ile	Arg	His	Tyr	Val	Val
			325					330						335	
Cys	Ser	Thr	Pro	Gln	Ser	Gln	Tyr	Tyr	Leu	Ala	Glu	Lys	His	Leu	Phe
			340					345					350		
Ser	Thr	Ile	Pro	Glu	Leu	Ile	Asn	Tyr	His	Gln	His	Asn	Ser	Ala	Gly
		355					360					365			
Leu	Ile	Ser	Arg	Leu	Lys	Tyr	Pro	Val	Ser	Gln	Gln	Asn	Lys	Asn	Ala
	370					375					380				
Pro	Ser	Thr	Ala	Gly	Leu	Gly	Tyr	Gly	Ser	Trp	Glu	Ile	Asp	Pro	Lys
385				390						395					400
Asp	Leu	Thr	Phe	Leu	Lys	Glu	Leu	Gly	Thr	Gly	Gln	Phe	Gly	Val	Val
			405					410						415	
Lys	Tyr	Gly	Lys	Trp	Arg	Gly	Gln	Tyr	Asp	Val	Ala	Ile	Lys	Met	Ile
			420					425					430		
Lys	Glu	Gly	Ser	Met	Ser	Glu	Asp	Glu	Phe	Ile	Glu	Glu	Ala	Lys	Val
		435					440					445			
Met	Met	Asn	Leu	Ser	His	Glu	Lys	Leu	Val	Gln	Leu	Tyr	Gly	Val	Cys
	450					455					460				
Thr	Lys	Gln	Arg	Pro	Ile	Phe	Ile	Ile	Thr	Glu	Tyr	Met	Ala	Asn	Gly

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[illegible]

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met 1	Asn	Asn	Phe	Ile 5	Leu	Leu	Glu	Glu	Gln 10	Leu	Ile	Lys	Lys	Ser 15	Gln
Gln	Lys	Arg	Arg 20	Thr	Ser	Pro	Ser	Asn 25	Phe	Lys	Val	Arg	Phe 30	Phe	Val
Leu	Thr	Lys 35	Ala	Ser	Leu	Ala	Tyr 40	Phe	Glu	Asp	Arg	His 45	Gly	Lys	Lys
Arg	Thr 50	Leu	Lys	Gly	Ser	Ile 55	Glu	Leu	Ser	Arg	Ile 60	Lys	Cys	Val	Glu
Ile 65	Val	Lys	Ser	Asp 70	Ile	Ser	Ile	Pro	Cys	His 75	Tyr	Lys	Tyr	Pro	Phe 80
Gln	Val	Val	His 85	Asp	Asn	Tyr	Leu	Leu	Tyr 90	Val	Phe	Ala	Pro	Asp 95	Arg
Glu	Ser	Arg	Gln 100	Arg	Trp	Val	Leu	Ala 105	Leu	Lys	Glu	Glu	Thr 110	Arg	Asn
Asn	Asn	Ser 115	Leu	Val	Pro	Lys	Tyr 120	His	Pro	Asn	Phe	Trp 125	Met	Asp	Gly
Lys	Trp 130	Arg	Cys	Cys	Ser	Gln 135	Leu	Glu	Lys	Leu	Ala 140	Thr	Gly	Cys	Ala
Gln 145	Tyr	Asp	Pro	Thr 150	Lys	Asn	Ala	Ser	Lys 155	Lys	Pro	Leu	Pro	Pro	Thr 160
Pro	Glu	Asp	Asn 165	Arg	Arg	Pro	Leu	Trp 170	Glu	Pro	Glu	Glu	Thr 175	Val	Val
Ile	Ala	Leu	Tyr 180	Asp	Tyr	Gln	Thr	Asn 185	Asp	Pro	Gln	Glu	Leu 190	Ala	Leu
Arg	Arg	Asn 195	Glu	Glu	Tyr	Cys	Leu 200	Leu	Asp	Ser	Ser	Glu 205	Ile	His	Trp
Trp	Arg 210	Val	Gln	Asp	Arg	Asn 215	Gly	His	Glu	Gly	Tyr 220	Val	Pro	Ser	Ser
Tyr 225	Leu	Val	Glu	Lys 230	Ser	Pro	Asn	Asn	Leu 235	Glu	Thr	Tyr	Glu	Trp	Tyr 240

66

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Asn Lys Ser Ile Ser Arg Asp Lys Ala Glu Lys Leu Leu Leu Asp Thr
245 250 255
Gly Lys Glu Gly Ala Phe Met Val Arg Asp Ser Arg Thr Ala Gly Thr
260 265 270
Tyr Thr Val Ser Val Phe Thr Lys Ala Val Val Ser Glu Asn Asn Pro
275 280 285
Cys Ile Lys His Tyr His Ile Lys Glu Thr Asn Asp Asn Pro Lys Arg
290 295 300
Tyr Tyr Val Ala Glu Lys Tyr Val Phe Asp Ser Ile Pro Leu Leu Ile
305 310 315 320
Asn Tyr His Gln His Asn Gly Gly Gly Leu Val Thr Arg Leu Arg Tyr
325 330 335
Pro Val Cys Phe Gly Arg Gln Lys Ala Pro Val Thr Ala Gly Leu Arg
340 345 350
Tyr Gly Lys Trp Val Ile Asp Pro Ser Glu Leu Thr Phe Val Gln Glu
355 360 365
Ile Gly Ser Gly Gln Phe Gly Leu Val His Leu Gly Tyr Trp Leu Asn
370 375 380
Lys Asp Lys Val Ala Ile Lys Thr Ile Arg Glu Gly Ala Met Ser Glu
385 390 395 400
Glu Asp Phe Ile Glu Glu Ala Glu Val Met Met Lys Leu Ser His Pro
405 410 415
Lys Leu Val Gln Leu Tyr Gly Val Cys Leu Glu Gln Ala Pro Ile Cys
420 425 430
Leu Val Phe Glu Phe Met Glu His Gly Cys Leu Ser Asp Tyr Leu Arg
435 440 445
Thr Gln Arg Gly Leu Phe Ala Glu Thr Leu Leu Gly Met Cys Leu
450 455 460
Asp Val Cys Glu Gly Met Ala Tyr Leu Glu Glu Ala Cys Val Ile His
465 470 475 480
Arg Asp Leu Ala Ala Arg Asn Cys Leu Val Gly Glu Asn Gln Val Ile
485 490 495
Lys Val Ser Asp Phe Gly Met Thr Arg Phe Val Leu Asp Asp Gln Tyr
500 505 510
Thr Ser Ser Thr Gly Thr Lys Phe Pro Val Lys Trp Ala Ser Pro Glu
515 520 525
Val Phe Ser Phe Ser Arg Tyr Ser Ser Lys Ser Asp Val Trp Ser Phe
530 535 540
Gly Val Leu Met Trp Glu Val Phe Ser Glu Gly Lys Ile Pro Tyr Glu
545 550 555 560
Asn Arg Ser Asn Ser Glu Val Val Glu Asp Ile Ser Thr Gly Phe Arg
565 570 575
Leu Tyr Lys Pro Arg Leu Ala Ser Thr His Val Tyr Gln Ile Met Asn
580 585 590
His Cys Trp Lys Glu Arg Pro Glu Asp Arg Pro Ala Phe Ser Arg Leu
595 600 605
Leu Arg Gln Leu Ala Glu Ile Ala Glu Ser Gly Leu
610 615 620

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Met Val Ser Phe Pro Val Lys Ile Asn Phe His Ser Ser Pro Gln
1 5 10 15
Ser Arg Asp Arg Trp Val Lys Lys Leu Lys Glu Glu Ile Lys Asn Asn
20 25 30
Asn Asn Ile Met Ile Lys Tyr His Pro Lys Phe Trp Ala Asp Gly Ser
35 40 45

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Cont.

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Tyr Gln Cys Cys Arg Gln Thr Glu Lys Leu Ala Pro Gly Cys Glu Lys
 50 55 60
 Tyr Asn Leu Phe Glu Ser Ser Ile Arg Lys Thr Leu Pro Pro Ala Pro
 65 70 75 80
 Glu Ile Lys Lys Arg Arg Pro Pro Pro Ile Pro Pro Glu Glu Glu
 85 90 95
 Asn Thr Glu Glu Ile Val Val Ala Met Tyr Asp Phe Gln Ala Thr Glu
 100 105 110
 Ala His Asp Leu Arg Leu Glu Arg Gly Gln Glu Tyr Ile Ile Leu Glu
 115 120 125
 Lys Asn Asp Leu His Trp Trp Arg Ala Arg Asp Lys Tyr Gly Trp Tyr
 130 135 140
 Cys Arg Asn Thr Asn Arg Ser Lys Ala Glu Gln Leu Leu Arg Thr Glu
 145 150 155 160
 Asp Lys Glu Gly Gly Phe Met Val Arg Asp Ser Ser Gln Pro Gly Leu
 165 170 175
 Tyr Thr Val Ser Leu Tyr Thr Lys Phe Gly Gly Glu Gly Ser Ser Gly
 180 185 190
 Phe Arg His Tyr His Ile Lys Glu Thr Ala Thr Ser Pro Lys Lys Tyr
 195 200 205
 Tyr Leu Ala Glu Lys His Ala Phe Gly Ser Ile Pro Glu Ile Ile Glu
 210 215 220
 Tyr His Lys His Asn Ala Ala Gly Leu Val Thr Arg Leu Arg Tyr Pro
 225 230 235 240
 Val Ser Thr Lys Gly Lys Asn Ala Pro Thr Thr Ala Gly Phe Ser Tyr
 245 250 255
 Asp Lys Trp Glu Ile Asn Pro Ser Glu Leu Thr Phe Met Arg Glu Leu
 260 265 270
 Gly Ser Gly Leu Phe Gly Val Val Arg Leu Gly Lys Trp Arg Ala Gln
 275 280 285
 Tyr Lys Val Ala Ile Lys Ala Ile Arg Glu Gly Ala Met Cys Glu Glu
 290 295 300
 Asp Phe Ile Glu Glu Ala Lys Val Met Met Lys Leu Thr His Pro Lys
 305 310 315 320
 Leu Val Gln Leu Tyr Gly Val Cys Thr Gln Gln Lys Pro Ile Tyr Ile
 325 330 335
 Val Thr Glu Phe Met Glu Arg Gly Cys Leu Leu Asn Phe Leu Arg Gln
 340 345 350
 Arg Gln Gly His Phe Ser Arg Asp Met Leu Leu Ser Met Cys Gln Asp
 355 360 365
 Val Cys Glu Gly Met Glu Tyr Leu Glu Arg Asn Ser Phe Ile His Arg
 370 375 380
 Asp Leu Ala Ala Arg Asn Cys Leu Val Asn Glu Ala Gly Val Val Lys
 385 390 395 400
 Val Ser Asp Phe Gly Met Ala Arg Tyr Val Leu Asp Asp Gln Tyr Thr
 405 410 415
 Ser Ser Ser Gly Ala Lys Phe Pro Val Lys Trp Cys Pro Pro Glu Val
 420 425 430
 Phe Asn Tyr Ser Arg Phe Ser Ser Lys Ser Asp Val Trp Ser Phe Gly
 435 440 445
 Val Leu Met Trp Glu Ile Phe Thr Glu Gly Arg Met Pro Phe Glu Lys
 450 455 460
 Asn Thr Asn Tyr Glu Val Val Thr Met Val Thr Arg Gly His Arg Leu
 465 470 475 480
 His Arg Pro Lys Leu Ala Thr Lys Tyr Leu Tyr Glu Val Met Leu Arg
 485 490 495
 Cys Trp Gln Glu Arg Pro Glu Gly Arg Pro Ser Phe Glu Asp Leu Leu
 500 505 510
 Arg Thr Ile Asp Glu Leu Val Glu Cys Glu Glu Thr Phe Gly Arg
 515 520 525

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 537 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown

67

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met 1	Gly	Cys	Val	Gln 5	Cys	Lys	Asp	Lys	Glu 10	Ala	Thr	Lys	Leu	Thr 15	Glu
Glu	Arg	Asp	Gly 20	Ser	Leu	Asn	Gln	Ser 25	Ser	Gly	Tyr	Arg	Tyr 30	Gly	Thr
Asp	Pro	Thr 35	Pro	Gln	His	Tyr	Pro 40	Ser	Phe	Gly	Val	Thr 45	Ser	Ile	Pro
Asn	Tyr 50	Asn	Asn	Phe	His	Ala 55	Ala	Gly	Gly	Gln	Gly 60	Leu	Thr	Val	Phe
Gly 65	Gly	Val	Asn	Ser	Ser 70	Ser	His	Thr	Gly	Thr 75	Leu	Arg	Thr	Arg	Gly 80
Gly	Thr	Gly	Val 85	Thr	Leu	Phe	Val	Ala	Leu 90	Tyr	Asp	Tyr	Glu	Ala 95	Arg
Thr	Glu	Asp	Asp 100	Leu	Ser	Phe	His	Lys 105	Gly	Glu	Lys	Phe	Gln 110	Ile	Leu
Asn	Ser	Ser 115	Glu	Gly	Asp	Trp	Trp 120	Glu	Ala	Arg	Ser	Leu 125	Thr	Thr	Gly
Glu	Thr 130	Gly	Tyr	Ile	Pro	Ser 135	Asn	Tyr	Val	Ala	Pro 140	Val	Asp	Ser	Ile
Gln 145	Ala	Glu	Glu	Trp	Tyr 150	Phe	Gly	Lys	Leu	Gly 155	Arg	Lys	Asp	Ala	Glu 160
Arg	Gln	Leu	Leu 165	Ser	Phe	Gly	Asn	Pro	Arg 170	Gly	Thr	Phe	Leu 175	Ile	Arg
Glu	Ser	Glu	Thr 180	Thr	Lys	Gly	Ala	Tyr 185	Ser	Leu	Ser	Ile	Arg 190	Asp	Trp
Asp	Asp	Met 195	Lys	Gly	Asp	His	Val 200	Lys	His	Tyr	Lys	Ile 205	Arg	Lys	Leu
Asp	Asn 210	Gly	Gly	Tyr	Tyr 215	Ile	Thr	Thr	Arg	Ala	Gln 220	Phe	Glu	Thr	Leu
Gln 225	Gln	Leu	Val	Gln	His 230	Tyr	Ser	Glu	Arg	Ala 235	Ala	Gly	Leu	Cys	Cys 240
Arg	Leu	Val	Val 245	Pro	Cys	His	Lys	Gly	Met 250	Pro	Arg	Leu	Thr	Asp 255	Leu
Ser	Val	Lys	Thr 260	Lys	Asp	Val	Trp	Glu	Ile 265	Pro	Arg	Glu	Ser 270	Leu	Gln
Leu	Ile	Lys 275	Arg	Leu	Gly	Asn	Gly 280	Gln	Phe	Gly	Glu	Val 285	Trp	Met	Gly
Thr	Trp 290	Asn	Gly	Asn	Thr	Lys 295	Val	Ala	Ile	Lys	Thr 300	Leu	Lys	Pro	Gly
Thr 305	Met	Ser	Pro	Glu	Ser 310	Phe	Leu	Glu	Glu	Ala 315	Gln	Ile	Met	Lys	Lys 320
Leu	Lys	His	Asp 325	Lys	Leu	Val	Gln	Leu	Tyr 330	Ala	Val	Val	Ser	Glu 335	Glu
Pro	Ile	Tyr 340	Ile	Val	Thr	Glu	Tyr	Met 345	Asn	Lys	Gly	Ser	Leu 350	Leu	Asp
Phe	Leu	Lys 355	Asp	Gly	Glu	Gly	Arg 360	Ala	Leu	Lys	Leu	Pro 365	Asn	Leu	Val
Asp	Met 370	Ala	Ala	Gln	Val	Ala 375	Ala	Gly	Met	Ala	Tyr 380	Ile	Glu	Arg	Met
Asn 385	Tyr	Ile	His	Arg	Asp 390	Leu	Arg	Ser	Ala	Asn 395	Ile	Leu	Val	Gly	Asn 400
Gly	Leu	Ile	Cys 405	Lys	Ile	Ala	Asp	Phe	Gly 410	Leu	Ala	Arg	Leu	Ile 415	Glu
Asp	Asn	Glu	Tyr 420	Thr	Ala	Arg	Gln	Gly 425	Ala	Lys	Phe	Pro	Ile 430	Lys	Trp
Thr	Ala	Pro 435	Glu	Ala	Ala	Leu	Tyr 440	Gly	Arg	Phe	Thr	Ile 445	Lys	Ser	Asp
Val	Trp 450	Ser	Phe	Gly	Ile	Leu 455	Leu	Thr	Glu	Leu	Val 460	Thr	Lys	Gly	Arg
Val 465	Pro	Tyr	Pro	Gly	Met 470	Asn	Asn	Arg	Glu	Val 475	Leu	Glu	Gln	Val	Glu 480
Arg	Gly	Tyr	Arg	Met	Pro	Cys	Pro	Gln	Asp	Cys	Pro	Ile	Ser	Leu	His

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				485					490					495		
Glu	Leu	Met	Ile	His	Cys	Trp	Lys	Lys	Asp	Pro	Glu	Glu	Arg	Pro	Thr	
			500					505					510			
Phe	Glu	Tyr	Leu	Gln	Ser	Phe	Leu	Glu	Asp	Tyr	Phe	Thr	Ala	Thr	Glu	
		515					520					525				
Pro	Gln	Tyr	Gln	Pro	Gly	Glu	Asn	Leu								
	530					535										

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Gly	Cys	Val	His	Cys	Lys	Glu	Lys	Ile	Ser	Gly	Lys	Gly	Gln	Gly	
1				5					10					15		
Gly	Ser	Gly	Thr	Gly	Thr	Pro	Ala	His	Pro	Pro	Ser	Gln	Tyr	Asp	Pro	
			20					25					30			
Asp	Pro	Thr	Gln	Leu	Ser	Gly	Ala	Phe	Thr	His	Ile	Pro	Asp	Phe	Asn	
		35					40					45				
Asn	Phe	His	Ala	Ala	Ala	Val	Ser	Pro	Pro	Val	Pro	Phe	Ser	Gly	Pro	
	50					55					60					
Gly	Phe	Tyr	Pro	Cys	Asn	Thr	Leu	Gln	Ala	His	Ser	Ser	Ile	Thr	Gly	
65				70					75					80		
Gly	Gly	Val	Thr	Leu	Phe	Ile	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr	
			85					90						95		
Glu	Asp	Asp	Leu	Ser	Phe	Gln	Lys	Gly	Glu	Lys	Phe	His	Ile	Ile	Asn	
			100					105					110			
Asn	Thr	Glu	Gly	Asp	Trp	Trp	Glu	Ala	Arg	Ser	Leu	Ser	Ser	Gly	Ala	
		115					120					125				
Thr	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Val	Asp	Ser	Ile	Gln	
	130					135					140					
Ala	Glu	Glu	Trp	Tyr	Phe	Gly	Lys	Ile	Gly	Arg	Lys	Asp	Ala	Glu	Arg	
145					150					155					160	
Gln	Leu	Leu	Cys	His	Gly	Asn	Cys	Arg	Gly	Thr	Phe	Leu	Ile	Arg	Glu	
			165					170						175		
Ser	Glu	Thr	Thr	Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	
		180						185					190			
Glu	Ala	Lys	Gly	Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	
		195					200					205				
Ser	Gly	Gly	Tyr	Tyr	Ile	Thr	Thr	Arg	Ala	Gln	Phe	Asp	Thr	Ile	Gln	
	210					215					220					
Gln	Leu	Val	Gln	His	Tyr	Ile	Glu	Arg	Ala	Ala	Gly	Leu	Cys	Cys	Arg	
225				230					235						240	
Leu	Ala	Val	Pro	Cys	Pro	Lys	Gly	Thr	Pro	Lys	Leu	Ala	Asp	Leu	Ser	
			245					250						255		
Val	Lys	Thr	Lys	Asp	Val	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Gln	Leu	
		260						265						270		
Leu	Gln	Lys	Leu	Gly	Asn	Gly	Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Thr	
	275					280						285				
Trp	Asn	Gly	Thr	Thr	Lys	Val	Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	
	290				295						300					
Met	Ser	Pro	Glu	Ala	Phe	Leu	Glu	Glu	Ala	Gln	Ile	Met	Lys	Arg	Leu	
305					310					315					320	
Arg	His	Asp	Lys	Leu	Val	Gln	Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro	
			325						330					335		
Ile	Tyr	Ile	Val	Thr	Glu	Phe	Met	Ser	Gln	Gly	Ser	Leu	Leu	Asp	Phe	
		340					345						350			
Leu	Lys	Asp	Gly	Asp	Gly	Arg	Tyr	Leu	Lys	Leu	Pro	Gln	Leu	Val	Asp	
	355					360						365				
Met	Ala	Ala	Gln	Ile	Ala	Ala	Gly	Met	Ala	Tyr	Ile	Glu	Arg	Met	Asn	

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(xi) SEQUENCE DESCRIPTION: SEO ID NO:13:

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Glu	Val	Lys	260	Leu	Gly	Gln	Gly	Cys	265	Phe	Gly	Glu	Val	Trp	270	Met	Gly	Thr
Trp	Asn	Gly	275	Thr	Thr	Arg	Val	Ala	280	Ile	Lys	Thr	Leu	Lys	285	Pro	Gly	Thr
Met	Ser	Pro	290	Glu	Ala	Phe	Leu	Gln	295	Glu	Ala	Gln	Val	Met	300	Lys	Lys	Leu
Arg	His	Glu	305	Lys	Leu	Val	Gln	Leu	310	Tyr	Ala	Val	Val	Ser	315	Glu	Glu	Pro
Ile	Tyr	Ile	325	Val	Thr	Glu	Tyr	Met	330	Ser	Lys	Gly	Ser	Leu	335	Leu	Asp	Phe
Leu	Lys	Gly	340	Glu	Thr	Gly	Lys	Tyr	345	Leu	Arg	Leu	Pro	Gln	350	Leu	Val	Asp
Met	Ala	Ala	355	Gln	Ile	Ala	Ser	Gly	360	Met	Ala	Tyr	Val	Glu	365	Arg	Met	Asn
Tyr	Val	His	370	Arg	Asp	Leu	Arg	Ala	375	Ala	Asn	Ile	Leu	Val	380	Gly	Glu	Asn
Leu	Val	Cys	385	Lys	Val	Ala	Asp	Phe	390	Gly	Leu	Ala	Arg	Leu	395	Ile	Glu	Asp
Asn	Glu	Tyr	405	Thr	Ala	Arg	Gln	Gly	410	Ala	Lys	Phe	Pro	Ile	415	Lys	Trp	Thr
Ala	Pro	Glu	420	Ala	Ala	Leu	Tyr	Gly	425	Arg	Phe	Thr	Ile	Lys	430	Ser	Asp	Val
Trp	Ser	Phe	435	Gly	Ile	Leu	Leu	Thr	440	Glu	Leu	Thr	Thr	Lys	445	Gly	Arg	Val
Pro	Tyr	Pro	450	Gly	Met	Val	Asn	Arg	455	Glu	Val	Leu	Asp	Gln	460	Val	Glu	Arg
Gly	Tyr	Arg	465	Met	Pro	Cys	Pro	Pro	470	Glu	Cys	Pro	Glu	Ser	475	Leu	His	Asp
Leu	Met	Cys	485	Gln	Cys	Trp	Arg	Lys	490	Glu	Pro	Glu	Glu	Arg	495	Pro	Thr	Phe
Glu	Tyr	Leu	500	Gln	Ala	Phe	Leu	Glu	505	Asp	Tyr	Phe	Thr	Ser	510	Thr	Glu	Pro
Gln	Tyr	Gln	515	Pro	Gly	Glu	Asn	Leu	520						525			
			530						535									

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Gly	Cys	Ile	Lys	Ser	Lys	Glu	Asn	Lys	Ser	Pro	Ala	Ile	Lys	Tyr
1				5					10					15	
Arg	Pro	Glu	Asn	Thr	Pro	Glu	Pro	Val	Ser	Thr	Ser	Val	Ser	His	Tyr
			20					25					30		
Gly	Ala	Glu	Pro	Thr	Thr	Val	Ser	Pro	Cys	Pro	Ser	Ser	Ser	Ala	Lys
		35					40					45			
Gly	Thr	Ala	Val	Asn	Phe	Ser	Ser	Leu	Ser	Met	Thr	Pro	Phe	Gly	Gly
	50				55					60					
Ser	Ser	Gly	Val	Thr	Pro	Phe	Gly	Gly	Ala	Ser	Ser	Ser	Phe	Ser	Val
65				70					75					80	
Val	Pro	Ser	Ser	Tyr	Pro	Ala	Gly	Leu	Thr	Gly	Gly	Val	Thr	Ile	Phe
			85					90					95		
Val	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr	Thr	Glu	Asp	Leu	Ser	Phe
			100					105					110		
Lys	Lys	Gly	Glu	Arg	Phe	Gln	Ile	Ile	Asn	Asn	Thr	Glu	Gly	Asp	Trp
		115					120					125			
Trp	Glu	Ala	Arg	Ser	Ile	Ala	Thr	Gly	Lys	Asn	Gly	Tyr	Ile	Pro	Ser
	130					135					140				
Asn	Tyr	Val	Ala	Pro	Ala	Asp	Ser	Ile	Gln	Ala	Glu	Glu	Trp	Tyr	Phe

145 150 155 160
 Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
 165 170 175
 Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
 180 185 190
 Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
 195 200 205
 Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
 210 215 220
 Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
 225 230 235 240
 Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
 245 250 255
 Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
 260 265 270
 Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
 275 280 285
 Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
 290 295 300
 Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
 305 310 315 320
 Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
 325 330 335
 Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser
 340 345 350
 Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
 355 360 365
 Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
 370 375 380
 Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 385 390 395 400
 Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
 405 410 415
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
 420 425 430
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
 435 440 445
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
 450 455 460
 Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
 465 470 475 480
 Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
 485 490 495
 Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
 500 505 510
 Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
 515 520 525
 Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535 540

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
 1 5 10 15
 Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
 20 25 30
 His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala

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- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Gly	Cys	Ile	Lys	Ser	Lys	Gly	Lys	Asp	Ser	Leu	Ser	Asp	Asp	Gly
1				5					10				15		
Val	Asp	Leu	Lys	Thr	Gln	Pro	Val	Arg	Asn	Thr	Glu	Arg	Thr	Ile	Tyr
			20					25					30		
Val	Arg	Asp	Pro	Thr	Ser	Asn	Lys	Gln	Gln	Arg	Pro	Val	Pro	Glu	Ser
		35					40					45			
Gln	Leu	Leu	Pro	Gly	Gln	Arg	Phe	Gln	Thr	Lys	Asp	Pro	Glu	Glu	Gln
	50					55					60				
Gly	Asp	Ile	Val	Val	Ala	Leu	Tyr	Pro	Tyr	Asp	Gly	Ile	His	Pro	Asp
65					70					75					80
Asp	Leu	Ser	Phe	Lys	Lys	Gly	Glu	Lys	Met	Lys	Val	Leu	Glu	Glu	His
				85					90					95	
Gly	Glu	Trp	Trp	Lys	Ala	Lys	Ser	Leu	Leu	Thr	Lys	Lys	Glu	Gly	Phe
			100					105					110		
Ile	Pro	Ser	Asn	Tyr	Val	Ala	Lys	Leu	Asn	Thr	Leu	Glu	Thr	Glu	Glu
		115					120					125			
Trp	Phe	Phe	Lys	Asp	Ile	Thr	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu
	130					135					140				
Ala	Pro	Gly	Asn	Ser	Ala	Gly	Ala	Phe	Leu	Ile	Arg	Glu	Ser	Glu	Thr
145					150					155					160
Leu	Lys	Gly	Ser	Phe	Ser	Leu	Ser	Val	Arg	Asp	Phe	Asp	Pro	Val	His
				165					170					175	
Gly	Asp	Val	Ile	Lys	His	Tyr	Lys	Ile	Arg	Ser	Leu	Asp	Asn	Gly	Gly
			180					185					190		
Tyr	Tyr	Ile	Ser	Pro	Arg	Ile	Thr	Phe	Pro	Cys	Ile	Ser	Asp	Met	Ile
		195					200					205			
Lys	His	Tyr	Gln	Lys	Gln	Ala	Asp	Gly	Leu	Cys	Arg	Arg	Leu	Glu	Lys
	210					215					220				
Ala	Cys	Ile	Ser	Pro	Lys	Pro	Gln	Lys	Pro	Trp	Asp	Lys	Asp	Ala	Trp
225					230					235					240
Glu	Ile	Pro	Arg	Glu	Ser	Ile	Lys	Leu	Val	Lys	Arg	Leu	Gly	Ala	Gly
				245					250					255	
Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Tyr	Tyr	Asn	Asn	Ser	Thr	Lys	Val
			260					265					270		
Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Val	Gln	Ala	Phe	Leu
		275					280					285			
Glu	Glu	Ala	Asn	Leu	Met	Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Arg
	290					295					300				
Leu	Tyr	Ala	Val	Val	Thr	Arg	Glu	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu
305					310					315					320
Tyr	Met	Ala	Lys	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Ser	Asp	Glu	Gly
				325					330					335	
Gly	Lys	Val	Leu	Leu	Pro	Lys	Leu	Ile	Asp	Phe	Ser	Ala	Gln	Ile	Ala
			340					345					350		
Glu	Gly	Met	Ala	Tyr	Ile	Glu	Arg	Lys	Asn	Tyr	Ile	His	Arg	Asp	Leu
		355					360					365			
Arg	Ala	Ala	Asn	Val	Leu	Val	Ser	Glu	Ser	Leu	Met	Cys	Lys	Ile	Ala
	370					375					380				
Asp	Phe	Gly	Leu	Ala	Arg	Val	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg
385					390					395					400
Glu	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn
				405					410					415	
Phe	Gly	Cys	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu
			420					425					430		
Leu	Tyr	Glu	Ile	Val	Thr	Tyr	Gly	Lys	Ile	Pro	Tyr	Pro	Gly	Arg	Thr
		435					440					445			
Asn	Ala	Asp	Val	Met	Thr	Ala	Leu	Ser	Gln	Gly	Tyr	Arg	Met	Pro	Arg
	450					455					460				

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		435					440					445					
Asn	Ala	Asp	Val	Met	Thr	Ala	Leu	Ser	Gln	Gly	Tyr	Arg	Met	Pro	Arg		
	450					455					460						
Val	Glu	Asn	Cys	Pro	Asp	Glu	Leu	Tyr	Asp	Ile	Met	Lys	Met	Cys	Trp		
465					470					475					480		
Lys	Glu	Lys	Ala	Glu	Glu	Arg	Pro	Thr	Phe	Asp	Tyr	Leu	Gln	Ser	Val		
			485						490					495			
Leu	Asp	Asp	Phe	Tyr	Thr	Ala	Thr	Glu	Gly	Gln	Tyr	Gln	Gln	Gln	Pro		
		500					505						510				

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Gly	Ser	Met	Lys	Ser	Lys	Phe	Leu	Gln	Val	Gly	Gly	Asn	Thr	Phe		
1				5					10					15			
Ser	Lys	Thr	Glu	Thr	Ser	Ala	Ser	Pro	His	Cys	Pro	Val	Tyr	Val	Pro		
			20					25					30				
Asp	Pro	Thr	Ser	Thr	Ile	Lys	Pro	Gly	Pro	Asn	Ser	His	Asn	Ser	Asn		
		35				40						45					
Thr	Pro	Gly	Ile	Arg	Glu	Ala	Gly	Ser	Glu	Asp	Ile	Ile	Val	Val	Ala		
50					55					60							
Leu	Tyr	Asp	Tyr	Glu	Ala	Ile	His	His	Glu	Asp	Leu	Ser	Phe	Gln	Lys		
65				70					75					80			
Gly	Asp	Gln	Met	Val	Val	Leu	Glu	Glu	Ser	Gly	Glu	Trp	Trp	Lys	Ala		
			85					90					95				
Arg	Ser	Leu	Ala	Thr	Arg	Lys	Glu	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val		
			100					105					110				
Ala	Arg	Val	Asp	Ser	Leu	Glu	Thr	Glu	Glu	Trp	Phe	Phe	Lys	Gly	Ile		
		115					120					125					
Ser	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ala	Pro	Gly	Asn	Met	Leu		
	130					135					140						
Gly	Ser	Phe	Met	Ile	Arg	Asp	Ser	Glu	Thr	Thr	Lys	Gly	Ser	Tyr	Ser		
145				150					155						160		
Leu	Ser	Val	Arg	Asp	Tyr	Asp	Pro	Arg	Gln	Gly	Asp	Thr	Val	Lys	His		
			165					170					175				
Tyr	Lys	Ile	Arg	Thr	Leu	Asp	Asn	Gly	Gly	Phe	Tyr	Ile	Ser	Pro	Arg		
		180					185						190				
Ser	Thr	Phe	Ser	Thr	Leu	Gln	Glu	Leu	Val	Asp	His	Tyr	Lys	Lys	Gly		
		195					200					205					
Asn	Asp	Gly	Leu	Cys	Gln	Lys	Leu	Ser	Val	Pro	Cys	Met	Ser	Ser	Lys		
	210					215					220						
Pro	Gln	Lys	Pro	Trp	Glu	Lys	Asp	Ala	Trp	Glu	Ile	Pro	Arg	Glu	Ser		
225					230					235				240			
Leu	Lys	Leu	Glu	Lys	Lys	Leu	Gly	Ala	Gly	Gln	Phe	Gly	Glu	Val	Trp		
			245						250					255			
Met	Ala	Thr	Tyr	Asn	Lys	His	Thr	Lys	Val	Ala	Val	Lys	Thr	Met	Lys		
		260					265						270				
Pro	Gly	Ser	Met	Ser	Val	Glu	Ala	Phe	Leu	Ala	Glu	Ala	Asn	Val	Met		
		275					280					285					
Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Lys	Leu	His	Ala	Val	Val	Thr		
	290					295					300						
Lys	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Phe	Met	Ala	Lys	Gly	Ser	Leu		
305					310				315					320			
Leu	Asp	Phe	Leu	Lys	Ser	Asp	Glu	Gly	Ser	Lys	Gln	Pro	Leu	Pro	Lys		
			325					330						335			
Leu	Ile	Asp	Phe	Ser	Ala	Gln	Ile	Ala	Glu	Gly	Met	Ala	Phe	Ile	Glu		
		340					345						350				
Gln	Arg	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala	Asn	Ile	Leu	Val		
		355					360					365					

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385	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn	Phe	Gly	Ser	Phe	Thr	Ile	Lys	400
					405					410						415	
	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu	Met	Glu	Ile	Val	Thr	Tyr	
				420					425							430	
	Gly	Arg	Ile	Pro	Tyr	Pro	Gly	Met	Ser	Asn	Pro	Glu	Val	Ile	Arg	Ala	
			435					440					445				
	Leu	Glu	Arg	Gly	Tyr	Arg	Met	Pro	Arg	Pro	Glu	Asn	Cys	Pro	Glu	Glu	
		450				455						460					
	Leu	Tyr	Asn	Ile	Met	Met	Arg	Cys	Trp	Lys	Asn	Arg	Pro	Glu	Glu	Arg	
465						470					475					480	
	Pro	Thr	Phe	Glu	Tyr	Ile	Gln	Ser	Val	Leu	Asp	Asp	Phe	Tyr	Thr	Ala	
				485						490						495	
	Thr	Glu	Ser	Gln	Tyr	Gln	Gln	Gln	Pro								
				500					505								

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Gly	Cys	Gly	Cys	Ser	Ser	His	Pro	Glu	Asp	Asp	Trp	Met	Glu	Asn	
1				5				10					15			
Ile	Asp	Val	Cys	Glu	Asn	Cys	His	Tyr	Pro	Ile	Val	Pro	Leu	Asp	Gly	
			20					25					30			
Lys	Gly	Thr	Leu	Leu	Ile	Arg	Asn	Gly	Ser	Glu	Val	Arg	Asp	Pro	Leu	
		35				40						45				
Val	Thr	Tyr	Glu	Gly	Ser	Asn	Pro	Pro	Ala	Ser	Pro	Leu	Gln	Asp	Asn	
		50				55					60					
Leu	Val	Ile	Ala	Leu	His	Ser	Tyr	Glu	Pro	Ser	His	Asp	Gly	Asp	Leu	
65					70					75					80	
Gly	Phe	Glu	Lys	Gly	Glu	Gln	Leu	Arg	Ile	Leu	Glu	Gln	Ser	Gly	Glu	
			85					90					95			
Trp	Trp	Lys	Ala	Gln	Ser	Leu	Thr	Thr	Gly	Gln	Glu	Gly	Phe	Ile	Pro	
			100					105					110			
Phe	Asn	Phe	Val	Ala	Lys	Ala	Asn	Ser	Leu	Glu	Pro	Glu	Pro	Trp	Phe	
		115					120					125				
Phe	Lys	Asn	Leu	Ser	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ala	Pro	
	130					135					140					
Gly	Asn	Thr	His	Gly	Ser	Phe	Leu	Ile	Arg	Glu	Ser	Glu	Ser	Thr	Ala	
145					150					155					160	
Gly	Ser	Phe	Ser	Leu	Ser	Val	Arg	Asp	Phe	Asp	Gln	Asn	Gln	Gly	Glu	
			165					170					175			
Val	Val	Lys	His	Tyr	Lys	Ile	Arg	Asn	Leu	Asp	Asn	Gly	Gly	Phe	Tyr	
		180						185					190			
Ile	Ser	Pro	Arg	Ile	Thr	Phe	Pro	Gly	Leu	His	Glu	Leu	Val	Arg	His	
		195					200						205			
Tyr	Thr	Asn	Ala	Ser	Asp	Gly	Leu	Cys	Thr	Arg	Leu	Ser	Arg	Pro	Cys	
	210					215					220					
Gln	Thr	Gln	Lys	Pro	Gln	Lys	Pro	Trp	Trp	Glu	Asp	Glu	Trp	Glu	Val	
225					230					235					240	
Pro	Arg	Glu	Thr	Leu	Lys	Leu	Val	Glu	Arg	Leu	Gly	Ala	Gly	Gln	Phe	
			245					250					255			
Gly	Glu	Val	Trp	Met	Gly	Tyr	Tyr	Asn	Gly	His	Thr	Lys	Val	Ala	Val	
		260						265					270			
Lys	Ser	Leu	Lys	Gln	Gly	Ser	Met	Ser	Pro	Asp	Ala	Phe	Leu	Ala	Glu	
		275					280					285				
Ala	Asn	Leu	Met	Lys	Gln	Leu	Gln	His	Gln	Arg	Leu	Val	Arg	Leu	Tyr	
	290					295					300					
Ala	Val	Val	Thr	Gln	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Tyr	Met	Glu	
305					310					315					320	

290	Ala Val Val Thr Gln Glu	295	Pro Ile Tyr Ile Ile	300	Thr Glu Tyr Met Glu
305	Asn Gly Ser Leu Val Asp	310	Phe Leu Lys Thr Pro	315	Ser Gly Ile Lys Leu
	325		330		335
	Thr Ile Asn Lys Leu Leu		Asp Met Ala Ala Gln		Ile Ala Glu Gly Met
	340		345		350
	Ala Phe Ile Glu Glu Arg		Asn Tyr Ile His Arg		Asp Leu Arg Ala Ala
	355		360		365
	Asn Ile Leu Val Ser Asp		Thr Leu Ser Cys Lys		Ile Ala Asp Phe Gly
	370		375		380
	Leu Ala Arg Leu Ile Glu		Asp Asn Glu Tyr Thr		Ala Arg Glu Gly Ala
	385		390		395
	Lys Phe Pro Ile Lys Trp		Thr Ala Pro Glu Ala		Ile Asn Tyr Gly Thr
	405		410		415
	Phe Thr Ile Lys Ser Asp		Val Trp Ser Phe Gly		Ile Leu Leu Thr Glu
	420		425		430
	Ile Val Thr His Gly Arg		Ile Pro Tyr Pro Gly		Met Thr Asn Pro Glu
	435		440		445
	Val Ile Gln Asn Leu Glu		Arg Gly Tyr Arg Met		Val Arg Pro Asp Asn
	450		455		460
	Cys Pro Glu Glu Leu Tyr		Gln Leu Met Arg Leu		Cys Trp Lys Glu Arg
	465		470		475
	Pro Glu Asp Arg Pro Thr		Phe Asp Tyr Leu Arg		Ser Val Leu Glu Asp
	485		490		495
	Phe Phe Thr Ala Thr Glu		Gly Gln Tyr Gln Pro		Gln Pro
	500		505		

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Gly	Leu	Leu	Ser	Ser	Lys	Arg	Gln	Val	Ser	Glu	Lys	Gly	Lys	Gly
1				5					10					15	
Trp	Ser	Pro	Val	Lys	Ile	Arg	Thr	Gln	Asp	Lys	Ala	Pro	Pro	Pro	Leu
			20					25					30		
Pro	Pro	Leu	Val	Val	Phe	Asn	His	Leu	Ala	Pro	Pro	Ser	Pro	Asn	Gln
		35				40						45			
Asp	Pro	Asp	Glu	Glu	Glu	Arg	Phe	Val	Val	Ala	Leu	Phe	Asp	Tyr	Ala
	50					55					60				
Ala	Val	Asn	Asp	Arg	Asp	Leu	Gln	Val	Leu	Lys	Gly	Glu	Lys	Leu	Gln
65					70					75					80
Val	Leu	Arg	Ser	Thr	Gly	Asp	Trp	Trp	Leu	Ala	Arg	Ser	Leu	Val	Thr
			85					90						95	
Gly	Arg	Glu	Gly	Tyr	Val	Pro	Ser	Asn	Phe	Val	Ala	Pro	Val	Glu	Thr
		100						105					110		
Leu	Glu	Val	Glu	Lys	Trp	Phe	Phe	Arg	Thr	Ile	Ser	Arg	Lys	Asp	Ala
		115					120					125			
Glu	Arg	Gln	Leu	Leu	Ala	Pro	Met	Asn	Lys	Ala	Gly	Ser	Phe	Leu	Ile
	130					135					140				
Arg	Glu	Ser	Glu	Ser	Asn	Lys	Gly	Ala	Phe	Ser	Leu	Ser	Val	Lys	Asp
145					150					155					160
Ile	Thr	Thr	Gln	Gly	Glu	Val	Val	Lys	His	Tyr	Lys	Ile	Arg	Ser	Leu
			165					170						175	
Asp	Asn	Gly	Gly	Tyr	Tyr	Ile	Ser	Pro	Arg	Ile	Thr	Phe	Pro	Thr	Leu
		180					185						190		
Gln	Ala	Leu	Val	Gln	His	Tyr	Ser	Lys	Lys	Gly	Asp	Gly	Leu	Cys	Gln
	195						200					205			
Lys	Leu	Thr	Leu	Pro	Cys	Val	Asn	Leu	Ala	Pro	Lys	Asn	Leu	Trp	Ala

Leu	Gly	Ser	Gly	Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Tyr	Tyr	Lys	Asn	
				245					250					255		
Asn	Met	Lys	Val	Ala	Ile	Lys	Thr	Leu	Lys	Glu	Gly	Thr	Met	Ser	Pro	
			260					265					270			
Glu	Ala	Phe	Leu	Gly	Glu	Ala	Asn	Val	Met	Lys	Thr	Leu	Gln	His	Glu	
		275					280					285				
Arg	Leu	Val	Arg	Leu	Tyr	Ala	Val	Val	Thr	Arg	Glu	Pro	Ile	Tyr	Ile	
	290					295					300					
Val	Thr	Glu	Tyr	Met	Ala	Arg	Gly	Cys	Leu	Leu	Asp	Phe	Leu	Lys	Thr	
305					310				315						320	
Asp	Glu	Gly	Ser	Arg	Leu	Ser	Leu	Pro	Arg	Leu	Ile	Asp	Met	Ser	Ala	
			325					330						335		
Gln	Val	Ala	Glu	Gly	Met	Ala	Tyr	Ile	Glu	Arg	Met	Asn	Ser	Ile	His	
		340					345					350				
Arg	Asp	Leu	Arg	Ala	Ala	Asn	Ile	Leu	Val	Ser	Glu	Thr	Leu	Cys	Cys	
		355				360					365					
Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ile	Ile	Asp	Ser	Glu	Tyr	Thr	
	370					375					380					
Ala	Gln	Glu	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	
385					390					395					400	
Ile	His	Phe	Gly	Val	Phe	Thr	Ile	Lys	Ala	Asp	Val	Trp	Ser	Phe	Gly	
			405					410						415		
Val	Leu	Leu	Met	Val	Ile	Val	Thr	Tyr	Gly	Arg	Val	Pro	Tyr	Pro	Gly	
			420				425						430			
Met	Ser	Asn	Pro	Glu	Val	Ile	Arg	Ser	Leu	Glu	His	Gly	Tyr	Arg	Met	
		435					440					445				
Pro	Cys	Pro	Glu	Thr	Cys	Pro	Pro	Glu	Leu	Tyr	Asn	Asp	Ile	Ile	Thr	
	450					455					460					
Glu	Cys	Trp	Arg	Gly	Arg	Pro	Glu	Glu	Arg	Pro	Thr	Phe	Glu	Phe	Leu	
465					470				475						480	
Gln	Ser	Val	Leu	Glu	Asp	Phe	Tyr	Thr	Ala	Thr	Glu	Gly	Gln	Tyr	Glu	
				485					490					495		
Leu	Gln	Pro														

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAATTCCCA CAGNGACTTN GCNGCNAG

28

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCGA ANGTCANAC GTCNGA

26

C

78